Figure 1
Fatty Acid Biosynthetic Pathway
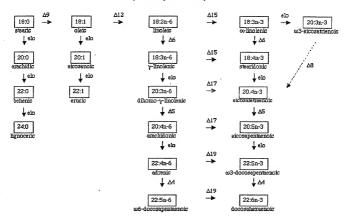
Figure 2

Gene Sequence of Delta 6- Desaturase from *Saprolegnia diclina* (ATCC 56851)

```
   1   ATGGTCCAGG GGCAAAAGGC CGAGAAGATC TCGTGGGCGA CCATCCGTGA
  51   GCACAACCGC CAAGACAACG CGTGGATCGT GATCCACCAC AAGGTGTACG
 101   ACATCTCGGC CTTTGAGGAC CACCCGGGCG GCGTCGTCAT GTTCACGCAG
 151   GCCGGCGAAG ACBCGACCGA TGGGTTCGCT GTCTTCCACC CGAGCTCGGC
 201   GCTCAAGCTC CTCGAGCAGT ACTACGTCGG CGACGTCGAC CAGTCGACGG
 251   CGGCCGTCGA CACGTCGATC TCGGACGAGG TCAAGAAGAG CCAGTCGGAC
 301   TTCATTGCGT CGTACCGCAA GCTGCGCCTT GAAGTCAAGC GCCTCGGCTT
 351   GTACGACTCG AGCAAGCTCT ACTACCTCTA CAAGTGCGCC TCGACGCTGA
 401   GCATTGCGCT TGTGTCGGCG GCCATTTGCC TCCACTTTGA CTCGACGGCC
 451   ATGTACATGG TCGCGGCTGT CATCCTTGGC CTCTTTTACC AGCAGTGCGG
 501   CTGGCTCGCC CATGACTTTC TGCACCACCA AGTGTTTGAG AACCACTTGT
 551   TTGGCGACCT CGTCGGCGTC ATGGTCGGCA ACCTCTGGCA GGGCTTCTCG
 601   GTGCAGTGGT GGAAGAACAA GCACAACACG CACCATGCGA TCCCCAACCT
 651   CCAGCCGACG CCCGAGATCG CCTTCCACGG CGACCCGGAC ATTGACACGA
 701   TGCCGAATTCT CGCGTGGTCG CTCAAGATGG CGCAGCACGC GGTCGACTCG
 751   CCCGTCGGGC TCTTCTTCAT GCGCTACCAA GCGTACCTGT ACTTTCCCAT
 801   CTTGCTCTTT GCGCGTATCT CGTGGGTGAT CCAGTCGGCC ATGTACGCCT
 851   TCTACAACGT TGGGCCCGGC GGCACCTTTG ACAAGGTCCA GTACCCGCTG
 901   CTCGAGCGCG CCGGCCTCCT CCTCTACTAC GGCTGGAACC TCGGCCTTGT
 951   GTACGCAGCC AACATGTCGC TGCTCCAAGC GGCTGCGTTC CTCTTTGTGA
1001   GCCAGGCGTC GTGCGGCCTC TTCCTCGCGA TGGTCTTTAG CGTCGGCCAC
1051   AACGGCATGG AGGTCTTTGA CAAGGACAGC AAGCCCGATT TTTGGAAGCT
1101   GCAAGTGCTC TCGACGCGCA ACGTGACGTC GTCGCTCTGG ATCGACTGGT
1151   TCATGGGCGG CCTCAACTAC CAGATCGACC ACCACTTGTT CCCGATGGTG
1201   CCCCGGCACA ACCTCCCGGC GCTCAACGTG CTCGTCAAGT CGCTCTGCAA
1251   GCAGTACGAC ATCCCATACC ACGAGACGGG CTTCATCGCG GGCATGGCCG
1301   AGGTCGTCGT GCACCTCGAG CGCATCGTCG TCGAGTTCTT CAAGGAGTTT
1351   CCCGCCATGT AA
```

Figure 3

Amino Acid Sequence of Delta 6- Desaturase from *Synechocystis dictica* (ATCC 56851)

```
  1    MVQGQKAEKI  SWATIREHNR  QDNAWIVIHH  KVYDISAFED  HPGGVVMFTQ
 51    AGEDATDAFA  VEHPSSALKL  LEQYYVGDVD  QSTAAVDTSI  SDEVKKSQSD
101    FIASYRKLRL  EVKRLGLYDS  SKLYYLYKCA  STLSLALYSA  AICLHFDSTA
151    MYMVAAYIIG  LFYQQCGWLA  HDEIHHQVEE  NHLEGDEVGV  MVGNLWQGES
201    VQWKKKHNT   HHAIPNIHAT  PEIAFHGDPD  IDTMPILAWS  LKMAQHAVDS
251    IVGLFEFMRVQ AYLYFPILIF  ARISWVIQSA  MYAFYNYGPG  GTEDKVQYPL
301    LERAGLLLYY  GWNLGLVYAA  NHSLLQAAAF  LFVSQASCGL  FLAMVFSVGH
351    NGMEVFIKDS  KPDEHKLQVL  STRNVTSSLH  IDWFMGGINY  QIDMHLFPMV
401    ERHNLPALNV  LVKSLCKQYD  IPYHLTGFIA  GMAFVVYHLE  RISIEEFKEF
451    PAM*
```

Figure 4

Gene Sequence of Delta 5- Desaturase from *Saprolegnia diclina* (ATCC 56851)

```
   1  ATGGCCCCGC AGACGGAGCT CCGCCAGCGC CACGCCGCCG TCGCCGAGAC
  51  GCCGGTGGCC GGCAAGAAGG CCTTTACATG GCAGGAGGTC GCGCAGCACA
 101  ACACGGCGGC CTCGGCCTGG ATCATTATCC GCGGCAAGGT CTACGAGGTG
 151  ACCGAGTGGG CCAACAAGCA CCCCGGCGGC CGCGAGATGG TGCTGCTGCA
 201  CGCCGGTCGC GAGGCCACCG ACACGTTCGA CTCGTACCAC CCGTTCAGCG
 251  ACAAGGCCGA GTCGATCTTG AACAAGTATG AGATTGGCAC GTTCACGGGC
 301  CCGTCCGAGT TTCCGACCTT CAAGCCGGAC ACGGGCTTCT ACAAGGAGTG
 351  CCGCAAGCGC GTTGGCGAGT ACTTCAAGAA GAACAACCTC CATCCGCAGG
 401  ACGGCTTCCC GGGCCTCTGG CGCATGATGG TCGTGTTTGC GGTCGCCGGC
 451  CTCGCCTTGT ACGGCATGCA CTTTTCGACT ATCTTTGCGC TGCAGCTCGC
 501  GGCCGCGGCG CTCTTTTGGCG TCTGCCAGGC GCTGCCGCTG CTCCACGTCA
 551  TGCACGACTC GTCGCACGCG TCGTACACCA ACATGCCGTT CTTCCATTAC
 601  GTCGTCGGCC GCTTTGCCAT GGACTGGTTT GCCGGCGGCT CGATGGTGTC
 651  ATGGCTCAAC CAGCACGTCG TGGGCCACCA CATCTACACG AACGTCGCGG
 701  GCTCGGACCC GGATCTTCCG GTCAACATGG ACGGCGACAT CCGCCGGATC
 751  GTGAACCGCC AGGTGTTCCA GCCCATGTAC GCATTCCAGC ACATCTACCT
 801  TCCGCCGCTC TATGGCGTGC TTGGCGTCAA GTTCGGCATC CAGGACTTCA
 851  CCGGACACGTT CGGGTCGCAC ACGAACGGCC CGATCCGCGT CAACCCGCAC
 901  GCGCTCTCGA CGTGGATGGC CATGGATCAGC TCCAAGTCGT TCTGGGCCTT
 951  CTACCGCGTG TACCTTCCGC TTGCCGTGCT CCAGATGCCC ATCAAGACGT
1001  ACCTTGCGAT CTTCTTCCTC GCCGAGTTTG TCACGGGCTG GTACCTCGCG
1051  TTCAACTTCC AAGTAAGCCA TGTCTCGACC GAGTGCGGCT ACCCATGCGG
1101  CGACGAGGCC AAGATGGCGC TCCAGGACGA GTGGGCAGTC TCGCAGGTCA
1151  AGACGTCGGT CGACTACGCC CATGGCTCGT GGATGACGAC GTTCCTTGCC
1201  GGCGGCGCTCA ACTACCAGGT CGTGCACCAC TTGTTCCCCA GCGTGTCGCA
1251  GTACCACTAC CCGGCGATCG CGCCCATCAT CGTCGACGTC TGCAAGGAGT
1301  ACAACATCAA GTACGCCATC TTGCCGGACT TTACGGCGGC GTTCGTTGCC
1351  CACTTGAAGC ACCTCCGCAA CATGGGCCAG CAGGGCATCG CCGCCACGAT
1401  CCACATGGGC TAA
```

Figure 5

Amino Acid Sequence of Delta 5- Desaturase from *Synechysis dixlius* (ATCC 56851)

```
1     MAPQTEIRQR HAAVAETFVA GKKAETMQEV AQHNTAASAM IIIRGKVYDV
51    TKWANKHPGG REMVLLHAGR EATDTEDSYM PESDKAESIL NKYYIGTETG
101   PSEPPTFKED TGFYKECRKR VGEYEKKNNL HPQDGEFGLW RMMYEAVAG
151   LALYGMMFST IFAIQLAAAA LFGVCQALPL LHYMMDSSHA SYTWMEFYHY
201   VVGREAMDWF AGGSMVSWIN QHVVGHHIYT NVAGSDPDLP VMMDGDIRRI
251   VNRQVEQPMY AFQMIYLPPL YGVIGIKERI QUETDTEGSH TNGFIRVNPN
301   ALSTWMAMIS SKSFWAYYRV YLPLAVLQMP IKTYLAIFF L AFFYTGWYLA
351   ENTQVSNVST ECGYPCGDEA KMAIQDEWAV SQVKTSVDYA HGSWMTTELA
401   GALNTQVVHH LFPSVSQYHY PAIAPIIVDV CKEYNIKYAI LPDFTAAFVA
451   HLKHIRNMGQ QGIAATIKME *
```

Figure 6

Gene Sequence of Delta 5- Desaturase from *Thraustochytrium aureum* (ATCC 34304)

```
   1   ATGGGACGCG  GCGGCGAAGG  TCAGGTGAAC  AGCGCGCAGG  TGGCACAAGG
  51   CGGTGCGGGA  ACGCGAAAGA  CGATCGTGAT  CGAGGGCTGGA  GTCTACGATG
 101   TCACCAACTT  TAGGCACCCC  GGCGGGTCGA  TCATCAAGTT  TCTCACGACC
 151   GACGGCACCG  AGGCTGTGGA  CGCGACGAAC  GCGTTTCGCG  AGTTTCACTG
 201   CCGGTCGGGC  AAGGCGGAAA  AGTACCTCAA  GAGCCTGCCC  AAGCTCGGCG
 251   CGCCGAGCAA  GATGAAGTTT  GAGCGCCAAGG  AGCAGGCCCG  GCGCGACGCG
 301   ATCACGCGAG  ACTACGTCAA  GCTGCGCGAG  GAGATGGTGG  CCGAGGGCCT
 351   CTTCAAGCCC  GCGCCCCTCC  ACATTGTCTA  CAGGTTTGCG  GAGATCGGAG
 401   CCCTGTTCGC  GGCCTCGTTC  TACCTGTTTT  CGATGCGCGG  AAACGTGTTC
 451   GCCACGCTCG  CGGCCATCGC  AGTCGGGGGC  ATCGCGCAGG  GCGCTGCGG
 501   CTGGCTCATG  CAGGAGTGCG  GACACTTCTC  GATGACCGGG  TACATCCCGC
 551   TTGACGTGCG  CCTGCAGGAG  CTGGTGTACG  GCGTGGGGTG  CTGGATGTCG
 601   GCGAGCTGGT  GGCGCGTTCA  GCACAACAAG  CACCACGCGA  CCCCGCAGAA
 651   ACTCAAGCAC  GACGTCGACC  TCGACACCCT  GCCGCTCGTT  GCGTTCAACG
 701   AGAAGATCGC  CGCCAAGGTG  CGCCCCGGCT  CGTTCCAGGC  CAAGTGGCTC
 751   TCGGCGCAGG  CGTACATTTT  TGGGCCGGTG  TCCTGCTTCC  TGGTTGGTCT
 801   CTTCTGGACC  CTGTTTCTGC  ACCCGCGCCA  CATGCGCGGC  ACGAGCCACT
 851   TTGCTGAGAT  GGCGGCCGTC  GCGGTGCGCG  TGTGGGCTG  GGCGGCGCTC
 901   ATGCACTCGT  TCGGGTACAG  CGGGAGCGAC  TCGTTCGGTC  TCTACATGGG
 951   CACGTTTGGC  TTTGGCTGCA  CCTACATCGT  CACCAACTTT  GCGGTCAGCC
1001   ACACGCACCT  CGACGTCACC  GAGCCGGACG  AGTTCCTGCA  CTGGGTCGAG
1051   TACGCCGCGC  TGCACACGAC  CAACGTGTCC  AACGACTCGT  GGTTCATCAC
1101   CTGGTGGATG  TCGTACCTCA  ACTTTCAGAT  CGAGCACCAC  CTCTTTCCGT
1151   CGCTGCCCCA  GCTCAACGCC  CCGCGCGTCG  CCCCGCGCGT  CCGCGCCCTC
1201   TTCGAGAAGC  ACGGCATGGC  TTACGACGAG  CGCCCGTACC  TTACGCGCGT
1251   TGGCGACACG  TTTGCCAACC  TGCACGCCGT  GGGCCAAAAC  GCGGGCCAGG
1301   CGGCGGCCAA  GGCGGCTTAG
```

Figure 7

Amino Acid Sequence of Delta 5- Desaturase from *Thraustochytrium aureum* (ATCC 34304)

```
  1   MGRGGEGQVN   SAQVAQGGAG   TRKTILIEGE   VYDVTNFRKP   GGSIIKFDTT
 51   DGTEAVDATN   AFREFHCRSG   KAEKYLKSLP   KLGAPSKMKF   DAKEQARRDA
101   ITRDYVKLRE   EMVAEGDFKP   APDHIVYREA   EIAALEAASF   YIFSMGNYE
151   ATLAAIAVGG   IAQGRCGWIM   HECGHFSMTG   YIFDVDRLQE   LVFGVGCSMS
201   ASWWRVQHNK   HHATPQKLKH   DVDLDTEPDV   AFNEKIAAKV   RPGSFQAKKL
251   SAQAYIFAPV   SCFFVGIFWT   LFIHERHMER   TSHFAEMAAV   AVRYVGWAAL
301   MHSFGYSGSD   SEGLYMATFG   FGCTYIFTMF   AVSHTHIDVT   E PDEF DHWYE
351   YAALHTTDVS   NDSWFITWHM   SYLNEQIEHH   LFPSLPQLNA   PRVAPRVRAL
401   FEKHGMAYDE   RPYLTALGDT   YANLHAVGGQ   AGQAAAKAA
```

Figure 8

```
   1  GAATTCACCA TGGGTCGCGG AGCACAGGGA GAGCCAGGC AGGCCACAGA
  51  GCTGAAGAGC AGCCCAAGTG AGCAGCGTAA GGTGTTGCTC ATTGACGGGC
 101  AGCTGTACGA TGCAACCAAC TTCAGGCATC CTGGTGGCTC CATCATCAAA
 151  TATTTGTGCA CCGATGGCAA GGAGTAGTT GATGCAACCG AAGCGTACAA
 201  GGAGTTCCAC TGCAGATCCT CGAAGGCGGT CAAGTACCTC AACTCCCTGC
 251  CAAAGATCGA CGGCCCAATC AAGTACAAAT ACGACGCAAA GGAGCAGGCT
 301  CGCCATGACA AACTCACGAG GGACTATGTA GCTCTCCGCA AACAGCTCGT
 351  CAAGGAGGGA TACTTTGACC CCAGCCCGCT CCACATTATC TACAGATGCG
 401  CCGAGTTGGC AGCCATGTTC GCTCTCTCGT TCTACCTTTT CTCCTTCAAG
 451  GGTAACGTCA TGGCCACTAT TGCTGCCATC GTGATTGGGG GGTGCGTGCA
 501  GGGTCGTTGT GGGTGGCTCA TGCATGAAGC TGGCCACTAC AGCATGACCG
 551  GAAACATCCC TGTTGACTTG CGCCTTCAAG AGTTTTTGTA CGGAATTGGG
 601  TGTGGCATGA GCGGGGCTTG GTGGAGAAGC CAGCACAACA AGCACCACGC
 651  CACCCCCCAA AAGCTCAAGC ATGACGTTGA TTTGGACACT CTTCCTCTTG
 701  TCGCCTGGAA CGGAGAAATT GCCCGTCGCG TCAAGCCAGG TAGCTTCCAG
 751  GCAAAGTGGC TTCATCTCCA GGGATACATC TTTGCCCCAG TCTCCTGCCT
 801  TCTCGTTGGT CTCTTCTGA CTTTGTACTT GCATCCTCGC CACATGATCC
 851  GCACCAAGCG CAACTTCGAG ATATTTTCTG TCGCTCTGCG CTAGTATGC
 901  TGGTTCTCGC TTCTTTTGAG CATGGGCTAC ACTGTCGGAG AGTCTCTGGG
 951  TCTCTATGTG CTTACTTTTG GACTTGGCTG TACCTACATC TTTACGCATT
1001  TTGCTGTAAG CCACACCCAC GCTGCACACC ACGAACGTTG CCATCGACTTG
1051  CACTGGGTCG AGTACGCTGC GCTGCACACC ACGAACGTTG CCATCGACTC
1101  GTACGTTGTC ACCTGGCTGA TGAGCTACCT CAACTTTCAG ATCGAGCACC
1151  ACTTGTTCCC TTGCTGCCCG CAGTTCCGCC ACCCTGCAAT CTCTTCTCGC
1201  GTCAAGAAAC TTTTCGAGGA CAATGGTCTG GTATACGACG CCCGCTCATA
1251  CGTCCAGCCG CTCAAGGATA CCTTCGGCAA CCTACACGAA GTGGGCGTCA
1301  ACGCTGGCCA AGCTGCCAAG AGCGAGTAAG ATCTCGAG
```

Start/stop underlined

Figure 9

```
  1  MGRGAQGEPR QATPLKSSPS EQRKVLLIDG QLYDATNFRH PGGSIIKYLC
 51  TDGKEVVDAT EAYKEFHCRS SKAVKYLNSL PKIDGPIKYK YDAKEQARHD
101  KLTREYVALR EQLVKEGYFD PSPLHIIYRC AELAAMFALS FYLFSFKGNV
151  MATIAAIVLG GCVQGRCGWL MHEAGHYSNT GNIPVDLRLQ EELYGICGCM
201  SGAWRSQHN KHHATPQKLK HDVDLDTLPL VAWNEKIARR VKPGSFQAKW
251  LHLQGYIFAP VSCLLVGLFW TLYLHPRHMI RTKRNFEIFS VALRYVCWFS
301  LLLSMGYTVG ESLGLYVLTF GLGCTVITTH FAVSHTHLPV SEEDEYLHWV
351  EYAALHTNV AIDSYVVTWL MSYLNFQIEH HLFPCCPQFR HPAISSRVEK
401  LFEDNGLVYD ARSYVQALKD TFGNLHEVGV NAGQAAKSE
```

Figure 10

```
   1  CCATGGGCCG CGGCGGCGAG AAAAGCGAGG TGGACCAGGT GCAGCCACAA
  51  AAGACCCGAGC AGCTCCAGAA GGCCAAGTGG GAGGATGTTG TTCGCATCAA
 101  TGGAGTCGAA TACGACCGTCA CGGACTATCT CAGAAAACAC CCTGGTGGCA
 151  GCGTGATCAA GTACGGGCTT GCCAACACCG GGCGCTGATGC CACGTCCCTC
 201  TTTGAGGCGT TCCACATGCG CTCAAAGAAG GCTCAGATGG TGCTCAAGTC
 251  TCTCCCAAAG CGTGCTCCGG TCCTCGAGAT CCAGCCAAAC CAGCTTCCAG
 301  AGGGAGCAGAC CAAGGAGGCG GAGATGCTGC GTGATTTTAA AAAATTTGAG
 351  GATGAGATTC GCCGGGATGG ATTGATGGAA CCTTCCTTCT GGCATGCGGC
 401  TTACAGATTA TCAGAGCTTG TAGGTATGTT CACGCTCGGC CTCTACCTCT
 451  TCTCGTTAAA CACTCCTTCTG TCTATTGCTG CTGGTGTCCT CGTCCACGGT
 501  CTCTTTGGTG CATTCTGTGG ATGGTGCCAG CATGAGGCAG GCCACGGCTC
 551  CTTTTTTAC AGCCTTTGGT GGGGCAAGCG TGTACAGGCC ATGTTGATCG
 601  GGTTTGGTCT AGGGACATCC GGCGACATGT GGAACCATGAT GCACAACAAG
 651  CATCATGCTG CCACCCAAAA GGTTCATCAC GACCTTGACA TTGACACAAC
 701  TCCTTTTGTA GCTTTCTTCA ACACTGCCATT TGAGAAAAAC AGATGGAAGG
 751  GCTTTTCCAA GGCTTGGGTC CGCTTTCAGG CTTTCACGTT CAATCCTGTC
 801  ACCAGCGGCA TGATCGTCAT GCTGTTCTGG CTGTTTTTTC TCCACCCTCG
 851  CCGCGTCGTT CAAAGAGAGA ACTTTGAGGA GGGTTTTTGG ATGCTGTCGA
 901  GCCACAITCGT GGGCACCTAT CTCTTCCACC TTGTGACCGG CTGGGAGAGC
 951  CTCGCTGCAT GCTACCTTGT TGGGTATTGG GCGTGCATGT GGGTGTCCGG
1001  TATGTATTTG TTTGGCCACT TTTCGCTCTC CCACACTCAT ATGGACATTG
1051  TGGAGGCGGA CGTGCATAAG AACTGGGTCA GGTACGCTGT TGACCACACT
1101  GTTGACATCA GCCCATCCAA CCCGCTCGTG TGCTGGGTCA TGGGTTACCT
1151  CAACATGCAG ACCATCCACC ACTTGTGGCC TGCCATGCCC CAGTACCACC
1201  AGGTCGAGGT CTCACGCCGC TTTGCCATCT TGCGCAAAAA ACACGGCCTC
1251  AACTACCGCG TCGTCTTCTTA CTTTGAGGCT TGGCGCCTGA TGCTCCAAAA
1301  TCTTGTCGAC GTCGGTTCCC ACTACCATGA GAACGGTGTC AAGCGCGCCC
1351  CAAAGAAAGC CAAGGCGCAG TAGAAAGCTA T
```

Start/stop underlined

Figure 11

```
  1  MGRGGEKSEV DQVQPQKTEQ LQKAKWEDVV RINGVEYDVT DYLRKHPGGS

 51  VIKYGLANTG ADATSLFEAF HMRSKKGQWV LKSLPKRAPV LEIQPNQLPE

101  EQTKEAEMLR DFKKFEDEIR RDGLMEPSFW HRAYRLSELV GMFTLGLYLF

151  SLNTPLSIHA GVLVHGLFGA FCGWCQHEAG HGSFTYSLWW GKRVQAMLIG

201  FGLGTSGDMW NMMHNKHHAA TQKVHHDLDI DTTPFVAFFN TAFEKNRWKG

251  FSKAWFQA FTFIPVTSGM IVMLFWLFFL HPRRVVQKKN FEEGFWNLSS

301  HIVRTYLFHL VTGWESLAAC YLVGYWACMW VSGWLFGHF SLSHTHMDIV

351  EADVHKNWVR YAVDHTVDIS PSNPLVCWVM GYLNMQTIHH LWPAMPQYHQ

401  VEVSRRFAIF AKKHGLNYRV VSYFEAWRLM LQNLADVGSH YHENGVKRAP

451  KKAKAQ
```

Figure 12

```
pRAT-2a    1    MGRGAQGEPRQATELKSSPSEQRKVLLIDGQLYDATNFRHPGGSI   45
pRAT-2c    1    MGRGAQGEPRQATELKSSPSEQRKVLLIDGQLYDATNFRHPGGSI   45

pRAT-2a    46   IKYLCTDGKEVVDATEAYKEFHCRSSKADKYLNSLPKIDGPIKYK   90
pRAT-2c    46   IKYLCTDGKEVVDATEAYKEFHCRSSKAVKYLNSLPKIDGPIKYK   90

pRAT-2a    91   YDAKEQARHDKLTREYVALREQLVKEGYFDPSPLHIIYRCAELAA   135
pRAT-2c    91   YDAKEQARHDKLTREYVALREQLVKEGYFDPSPLHIIYRCAELAA   135

pRAT-2a    136  MFALSFYLFSFKGNVVATIAAIVIGGCVQGRCGWLMHEAGHYSMT   180
pRAT-2c    136  MFALSFYLFSFKGNVMATIAAIVIGGCVQGRCGWLMHEAGHYSMT   180

pRAT-2a    181  GNIPVDLRLQEFLYGIGCGMSGAWWRRQHNKHHATPQKLKHDVDL   225
pRAT-2c    181  GNIPVDLRLQEFLYGIGCGMSGAWWRSQHNKHHATPQKLKHDVDL   225

pRAT-2a    226  DTLPLVAWNEKIARRVKPGSFQAKWPHLQGYIFAPVSCLLVGLFW   270
pRAT-2c    226  DTLPLVAWNEKIARRVKPGSFQAKWIHLQGYIFAPVSCLLVGLFW   270

pRAT-2a    271  TLYLHPRHMIRTKRNFEIFSVALRYVCWFSLLSMGYTVGESLGL   315
pRAT-2c    271  TLYLHPRHMIRTKRNFEIFSVALRYVCWFSLLSMGYTVGESLGL   315

pRAT-2a    316  YVLTFGLGCTYIFTHFAVSHTHLPVSEEDEYLHWVEYAALHTTNV   360
pRAT-2c    316  YVLTFGLGCTYIFTHFAVSHTHLPVSEEDEYLHWVEYAALHTTNV   360

pRAT-2a    361  AIDSYVVTWLMSYLNFQIEHHLFPCCPQFRHPAISSRVKKLFEDN   405
pRAT-2c    361  AIDSYVVTWLNFQIEHHLFPCCPQFRHPAISSRVKKLFEDN     405

pRAT-2a    406  GLVYDARSYVQALKDTFGNLHEVGVNAGQAAKSE   439
pRAT-2c    405  GLVYDARSYVQALKDTFGNLHEVGVNAGQAAKSE   439
```

Figure 13

```
pRAT-1a    1   MGRGGEKSEVDQVPQKTEQLQKAKWEDVVRINGVEYDVTDYLR   44
pRAT-1b    1   MGRGGEKSEVDQVPQKTEQLQKAKWEDVVRINGVEYDVTDYLR   44

pRAT-1a   45   KHPGGSVIKYGLANTGADATSLFEAFHMRSKKAQMVLKSLPKRA   88
pRAT-1b   45   KHPGGSVIKYGLANTGADATSLFEAFHMRSKKAQMVLKSLPKRA   88

pRAT-1a   89   PVLEIQPNQLPEEQTKEAEMLRDFKKFEDEIRRDGLMEPSFWHR  132
pRAT-1b   89   PVLEIQPNQLPEEQTKEAEMLRDFKKFEDEIRRDGLMEPSFWHR  132

pRAT-1a  133   AYRLSELVGMFTLGLYLFSLNTPLSIAAGVLVHGLFGAFCGWCQ  176
pRAT-1b  133   AYRLSELVGMFTLGLYLFSLNTPLSIAAGVLVHGLFGAFCGWCQ  176

pRAT-1a  177   HEAGHGSFFYSLWWGKRVQAMLIGFGLGTSGDMWNMMHNKHHAA  220
pRAT-1b  177   HEAGHGSFFYSLWWGKRVQAMLIGFGLGTSGDMWNVMHNKHHAA  220

pRAT-1a  221   TQKVHHDLDIDTTPFVAFFNTAFEKNRWKGFSKAWVRFQAFTFI  264
pRAT-1b  221   TQKVHHDLDIDTTPFVAFFNTAFEKNRWKGFSKAWVRFQAFTFI  264

pRAT-1a  265   PVTSGMIVMLFWLFFLHPRRVVQKKNFEEGFWMLSSHIVRTYLF  308
pRAT-1b  265   PVTSGMIVMLFWLFFLHPRRVVQKKNFEEGFWMLSSHIVRTYLF  308

pRAT-1a  309   HLVTGWESLAACYLVGYWACMWVSGMYLFGHFSLSHTHMDIVEA  352
pRAT-1b  309   HLVTGWESLAACYLVGYWACMWVSGMYLFGHFSLSHTHMDIVEA  352

pRAT-1a  353   DVHKNWVRYAVDHTVDISPSNPLVCWVMGYLNMQTIHHLWPAMP  396
pRAT-1b  353   DVHKNWVRYAVDHTVDISPSNPLVCWVMGYLNMQTIHHLWPAMP  396

pRAT-1a  397   QYHQVEVSRRFAIFAKKHGLNYRVVSYFEAWRLMLQNLADVGSH  440
pRAT-1b  397   QYHQVEVSRRFAIFAKKHGLNYRVVSYFEAWRLMLQNLADVGSH  440

pRAT-1a  441   YHENGVKRAPKKAKAQ  456
pRAT-1b  441   YHENGVKRAPKKAKAQ  456
```

Figure 14

```
   1   ATGGTGGCAG GCAAATCAGG CGCTGCGGCG CACGTGACTC ACAGCTCGAC
  51   ATTGCCCCGT GAGTACCATG GCGCGACCAA CGACTCGCGC TCTGAGGCGG
 101   CCGACGTCAC CGTCTCTAGC ATCGATGCTG AAAAGGAGAT GATCATCAAC
 151   GGCCGCGTGT ATGACGTGTC GTCATTTGTG AAGCGGCACC CAGGTGGCTC
 201   GGTGATCAAG TTCCAGCTGG GCGCCGACGC GAGCGACGCG TACAACAACT
 251   TTCACGTCCG CTCCAAGAAG GCGGACAAGA TGCTGTATTC GCTCCCGTCC
 301   CGGCCGGCCG AGGCCGGCTA CGCCCAGGAC GACATCTCCC GCGACTTTGA
 351   GAAGCTGCGC CTCGAGCTGA AGGAGGAGGG CTACTTCGAG CCCAACCTGG
 401   TGCACGTGAG CTACAGGTGT GTGGAGGTTC TTGCCATGTA CTGGGCTGGC
 451   GTCCAGCTCA TCTGGTCCGG GTACTGGTTC CTCGGCGCGA TCGTGGCCGG
 501   CATTGCGCAG GGCCGCTGCG GCTGGCTCCA GCATGAGGGT GGGCACTACT
 551   CGCTCACCGG CAACATCAAG ATCGACCGGC ATCTGCAGAT GGCCATCTAT
 601   GGGCTTGGCT GCGGCATGTC GGGCTGCTAC TGGCGCAACC AGCACAACAA
 651   GCACCACGCC ACGCCGCAGA AGCTCGGGAC CGACCCCGAC CTGCAGACGA
 701   TGCCGCTGGT GGCCTTCCAC AAGATCGTCG GCGCCAAGGC GCGAGGCAAG
 751   GGCAAGGCGT GGCTGGCGTG GCAGGCGCCG CTCTTCTTTG GCGGGATCAT
 801   CTGCTCGCTC GTCTCTTTCG GCTGGCAGTT CGTGCTCCAC CCCAACCACG
 851   CGCTGCGCGT GCACAATCAC CTGGAGCTCG CGTACATGGG CCTGCGGTAC
 901   GTGCTGTGGC ACCTGGCCTT TGGCCACCTC GGGCTGCTGA GCTCGCTCCG
 951   CCTGTACGCC TTTTACGTGG CCGTGGGCGG CACCTACATC TTCACCAACT
1001   TCGCCGTCTC GCACACCCAC AAGGACGTCG TCCCGCCCAC CAAGCACATC
1051   TCGTGGGCAC TCTACTCGGC CAACCACACG ACCAACTGCT CCGACTCGCC
1101   CTTTGTCAAC TGGTGGATGG CCTACCTCAA CTTCCAGATC GAGCACCACC
1151   TCTTCCCGTC GATGCCGCAG TACAACCACC CCAAGATCGC CCCGCGGGTG
1201   CGCGCGCTCT TCGAGAAGCA CGGGGTCGAG TATGACGTCC GGCCATACCT
1251   GGAGTGTTTT CGGGTCACGT ACGTCAACCT GCTCGCCGTA GGCAACCCGG
1301   AGCACTCCTA CCACGAGCAC ACGCACTAG
```

Figure 15

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  1   MVAGKSGAAA HVTHSSTLPR EYHGATNDSR SEAADVTVSS IDAEKEMIIN

 51   GRVYDVSSFV KRHPGGSVIK FQLGADASDA YNNFHVRSKK ADKMLYSLPS

101   RPAEAGYAQD DISRDFEKLR LELKEEGYFE PNLVHVSYRC VEVLAMYWAG

151   VQLIWSGYWF LGAIVAGIAQ GRCGWLQHEG GHYSLTGNIK IDRHLQMAIY

201   GLGCGMSGCY WRNQHNKHHA TPQKLGTDPD LQTMPLVAFH KIVGAKARGK

251   GKAWLAWQAP LFFGGIICSL VSFGWQFVLH PNHALRVHNH LELAYMGLRY

301   VLWHLAFGHL GLLSSLRLYA FYVAVGGTYI FTNFAVSHTH KDVVPPTKHI

351   SWALYSANHT TNCSDSPFVN WWMAYLNFQI EHHLFPSMPQ YNHPKIAPRV

401   RALFEKHGVE YDVRPYLECF RVTYVNLLAV GNPEHSYHEH TH
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